



PCT10

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/019,219

DATE: 06/12/2002
TIME: 12:21:40

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ENTERED

3 <110> APPLICANT: RONSIN, CHRISTOPHE
4 SCOTT, VERONIQUE
5 TRIEBEL, FREDERIC
7 <120> TITLE OF INVENTION: PEPTIDE COMPOUND DERIVED FROM A SHIFTED ORF OF THE ICE
8 GENE
10 <130> FILE REFERENCE: 065691-0263
12 <140> CURRENT APPLICATION NUMBER: 10/019,219
C--> 13 <141> CURRENT FILING DATE: 2002-05-15
15 <150> PRIOR APPLICATION NUMBER: PCT/FR00/01791
16 <151> PRIOR FILING DATE: 2000-06-27
18 <150> PRIOR APPLICATION NUMBER: FR 99/08224
19 <151> PRIOR FILING DATE: 1999-06-28
21 <160> NUMBER OF SEQ ID NOS: 8
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 162
27 <212> TYPE: PRT
28 <213> ORGANISM: Homo sapiens
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32 1 5 10 15
34 Cys Trp Leu Pro Trp Arg Thr Trp Trp Trp Ser Ser Ser Ser Thr Ala
35 20 25 30
37 Trp Val Ser Trp Ala Ser Ser Ala Leu Glu Thr Ser Thr Gln Pro Ala
38 35 40 45
40 Thr Gly Ala Thr Trp Thr Lys Trp Leu His Tyr Ala Gly Ser Ser Arg
41 50 55 60
43 Ile Ser Pro Thr Leu Glu Ala Thr Leu Thr Val Ser Pro Phe Leu Ala
44 65 70 75 80
46 Ser Leu Arg Val Ala Arg Val Cys Leu Arg Leu Leu Cys Pro Pro Tyr
47 85 90 95
49 Pro Lys Asp Ser Ser Thr Glu Pro Ser Trp Arg Val Ala Trp Pro Ser
50 100 105 110
52 Cys Pro Ala Ser Leu Pro Ala Gln Leu Met Ser Ser Pro Arg Trp Trp
53 115 120 125
55 Pro Thr Cys Leu Pro Val Thr Lys Leu Thr Leu Arg Pro Trp Trp Ala
56 130 135 140
58 Ala Cys Gly Ala Arg Val Lys Arg Arg Phe Leu Gln Leu Thr Ser Leu
59 145 150 155 160
61 Ser Arg
64 <210> SEQ ID NO: 2
65 <211> LENGTH: 9
66 <212> TYPE: PRT

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71 1 5
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75 <211> LENGTH: 521
76 <212> TYPE: DNA
77 <213> ORGANISM: Homo sapiens
79 <400> SEQUENCE: 3
80 acggtggtgc gcttgttttt ggcattggctt ccttgtatga tggttccatg ctggctgcct 60
81 tggagaacgt ggtggtggtc atcatccagt accgcctggg tgcctgggc ttcttcagca 120
82 ctggagacaa gcacgcaacc ggcaactggg gctacctgga ccaagtggct gcactacgct 180
83 ggggtccagca gaatatcgcc cactttggag gcaaccctga ccgtgtcacc atttttggcg 240
84 agtctgcggg tggcacgagt gtgtcttcgc ttgttgtgtc ccccatatcc caaggactct 300
85 tccacggagc catcatggag agtggcgtgg ccctcctgcc cggcctcatt gccagctcag 360
86 ctgatgtcat ctccacgggtg gtggccaacc tgtctgcctg tgaccaagtt gactctgagg 420
87 ccctggtggg ctgcctgcgg ggcaagagta aagaggagat tcttgcaatt aacaagcctt 480
88 tcaagatgat ccccgagtg gtggatggg tcttcctgcc c 521
91 <210> SEQ ID NO: 4
92 <211> LENGTH: 30
93 <212> TYPE: DNA
94 <213> ORGANISM: Artificial Sequence
96 <220> FEATURE:
97 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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100 cccaagcttg gtgaatagca gcgtgtccgc 30
103 <210> SEQ ID NO: 5
104 <211> LENGTH: 30
105 <212> TYPE: DNA
106 <213> ORGANISM: Artificial Sequence
108 <220> FEATURE:
109 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
111 <400> SEQUENCE: 5
112 tgctctagaa gggagctaca gctctgtgtg 30
115 <210> SEQ ID NO: 6
116 <211> LENGTH: 1680
117 <212> TYPE: DNA
118 <213> ORGANISM: Homo sapiens
120 <220> FEATURE:
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122 <222> LOCATION: (1)..(1677)
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126 Met Arg Leu His Arg Leu Arg Ala Arg Leu Ser Ala Val Ala Cys Gly
127 1 5 10 15
129 ctt ctg ctg ctt ctt gtc cgg ggc cag ggc cag gac tca gcc agt ccc 96
130 Leu Leu Leu Leu Leu Val Arg Gly Gln Gly Gln Asp Ser Ala Ser Pro
131 20 25 30
133 atc cgg acc aca cac acg ggg cag gtg ctg ggg agt ctt gtc cat gtg 144

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134 Ile Arg Thr Thr His Thr Gly Gln Val Leu Gly Ser Leu Val His Val
135          35          40          45
137 aag ggc gcc aat gcc ggg gtc caa acc ttc ctg gga att cca ttt gcc 192
138 Lys Gly Ala Asn Ala Gly Val Gln Thr Phe Leu Gly Ile Pro Phe Ala
139          50          55          60
141 aag cca cct cta ggt ccg ctg cga ttt gca ccc cct gag ccc cct gaa 240
142 Lys Pro Pro Leu Gly Pro Leu Arg Phe Ala Pro Pro Glu Pro Pro Glu
143          65          70          75          80
145 tct tgg agt ggt gtg agg gat gga acc acc cat ccg gcc atg tgt cta 288
146 Ser Trp Ser Gly Val Arg Asp Gly Thr Thr His Pro Ala Met Cys Leu
147          85          90          95
149 cag gac ctc acc gca gtg gag tca gag ttt ctt agc cag ttc aac atg 336
150 Gln Asp Leu Thr Ala Val Glu Ser Glu Phe Leu Ser Gln Phe Asn Met
151          100          105          110
153 acc ttc cct tcc gac tcc atg tct gag gac tgc ctg tac ctc agc atc 384
154 Thr Phe Pro Ser Asp Ser Met Ser Glu Asp Cys Leu Tyr Leu Ser Ile
155          115          120          125
157 tac acg ccg gcc cat agc cat gaa ggc tct aac ctg ccg gtg atg gtg 432
158 Tyr Thr Pro Ala His Ser His Glu Gly Ser Asn Leu Pro Val Met Val
159          130          135          140
161 tgg atc cac ggt ggt gcg ctt gtt ttt ggc atg gct tcc ttg tat gat 480
162 Trp Ile His Gly Gly Ala Leu Val Phe Gly Met Ala Ser Leu Tyr Asp
163          145          150          155          160
165 ggt tcc atg ctg gct gcc ttg gag aac gtg gtg gtg gtc atc atc cag 528
166 Gly Ser Met Leu Ala Ala Leu Glu Asn Val Val Val Val Ile Ile Gln
167          165          170          175
169 tac cgc ctg ggt gtc ctg ggc ttc ttc agc act gga gac aag cac gca 576
170 Tyr Arg Leu Gly Val Leu Gly Phe Phe Ser Thr Gly Asp Lys His Ala
171          180          185          190
173 acc ggc aac tgg ggc tac ctg gac caa gtg gct gca cta cgc tgg gtc 624
174 Thr Gly Asn Trp Gly Tyr Leu Asp Gln Val Ala Ala Leu Arg Trp Val
175          195          200          205
177 cag cag aat atc gcc cac ttt gga ggc aac cct gac cgt gtc acc att 672
178 Gln Gln Asn Ile Ala His Phe Gly Gly Asn Pro Asp Arg Val Thr Ile
179          210          215          220
181 ttt ggc gag tct gcg ggt ggc acg agt gtg tct tcg ctt gtt gtg tcc 720
182 Phe Gly Glu Ser Ala Gly Gly Thr Ser Val Ser Ser Leu Val Val Ser
183          225          230          235          240
185 ccc ata tcc caa gga ctc ttc cac gga gcc atc atg gag agt ggc gtg 768
186 Pro Ile Ser Gln Gly Leu Phe His Gly Ala Ile Met Glu Ser Gly Val
187          245          250          255
189 gcc ctc ctg ccc ggc ctc att gcc agc tca gct gat gtc atc tcc acg 816
190 Ala Leu Leu Pro Gly Leu Ile Ala Ser Ser Ala Asp Val Ile Ser Thr
191          260          265          270
193 gtg gtg gcc aac ctg tct gcc tgt gac caa gtt gac tct gag gcc ctg 864
194 Val Val Ala Asn Leu Ser Ala Cys Asp Gln Val Asp Ser Glu Ala Leu
195          275          280          285
197 gtg ggc tgc ctg cgg ggc aag agt aaa gag gag att ctt gca att aac 912
198 Val Gly Cys Leu Arg Gly Lys Ser Lys Glu Glu Ile Leu Ala Ile Asn

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199      290      295      300
201 aag cct ttc aag atg atc ccc gga gtg gtg gat ggg gtc ttc ctg ccc 960
202 Lys Pro Phe Lys Met Ile Pro Gly Val Val Asp Gly Val Phe Leu Pro
203 305      310      315      320
205 agg cac ccc cag gag ctg ctg gcc tct gcc gac ttt cag cct gtc cct 1008
206 Arg His Pro Gln Glu Leu Leu Ala Ser Ala Asp Phe Gln Pro Val Pro
207      325      330      335
209 agc att gtt ggt gtc aac aac aat gaa ttc ggc tgg ctc atc ccc aag 1056
210 Ser Ile Val Gly Val Asn Asn Asn Glu Phe Gly Trp Leu Ile Pro Lys
211      340      345      350
213 gtc atg agg atc tat gat acc cag aag gaa atg gac aga gag gcc tcc 1104
214 Val Met Arg Ile Tyr Asp Thr Gln Lys Glu Met Asp Arg Glu Ala Ser
215      355      360      365
217 cag gct gct ctg cag aaa atg tta acg ctg ctg atg ttg cct cct aca 1152
218 Gln Ala Ala Leu Gln Lys Met Leu Thr Leu Leu Met Leu Pro Pro Thr
219      370      375      380
221 ttt ggt gac ctg ctg agg gag gag tac att ggg gac aat ggg gat ccc 1200
222 Phe Gly Asp Leu Leu Arg Glu Glu Tyr Ile Gly Asp Asn Gly Asp Pro
223 385      390      395      400
225 cag acc ctc caa gcg cag ttc cag gag atg atg gcg gac tcc atg ttt 1248
226 Gln Thr Leu Gln Ala Gln Phe Gln Glu Met Met Ala Asp Ser Met Phe
227      405      410      415
229 gtg atc cct gca ctc caa gta gca cat ttt cag tgt tcc cgg gcc cct 1296
230 Val Ile Pro Ala Leu Gln Val Ala His Phe Gln Cys Ser Arg Ala Pro
231      420      425      430
233 gtg tac ttc tac gag ttc cag cat cag ccc agc tgg ctc aag aac atc 1344
234 Val Tyr Phe Tyr Glu Phe Gln His Gln Pro Ser Trp Leu Lys Asn Ile
235      435      440      445
237 agg cca ccg cac atg aag gca gac cat ggt gat gag ctt cct ttt gtt 1392
238 Arg Pro Pro His Met Lys Ala Asp His Gly Asp Glu Leu Pro Phe Val
239      450      455      460
241 ttc aga agt ttc ttt ggg ggc aac tac att aaa ttc act gag gaa gag 1440
242 Phe Arg Ser Phe Phe Gly Gly Asn Tyr Ile Lys Phe Thr Glu Glu Glu
243 465      470      475      480
245 gag cag cta agc agg aag atg atg aag tac tgg gcc aac ttt gcg aga 1488
246 Glu Gln Leu Ser Arg Lys Met Met Lys Tyr Trp Ala Asn Phe Ala Arg
247      485      490      495
249 aat ggg aac ccc aat ggc gag ggt ctg cca cac tgg ccg ctg ttc gac 1536
250 Asn Gly Asn Pro Asn Gly Glu Gly Leu Pro His Trp Pro Leu Phe Asp
251      500      505      510
253 cag gag gag caa tac ctg cag ctg aac cta cag cct gcg gtg ggc cgg 1584
254 Gln Glu Glu Gln Tyr Leu Gln Leu Asn Leu Gln Pro Ala Val Gly Arg
255      515      520      525
257 gct ctg aag gcc cac agg ctc cag ttc tgg aag aag gcg ctg ccc caa 1632
258 Ala Leu Lys Ala His Arg Leu Gln Phe Trp Lys Lys Ala Leu Pro Gln
259      530      535      540
261 aag atc cag gag ctc gag gag cct gaa gag aga cac aca gag ctg tag 1680
262 Lys Ile Gln Glu Leu Glu Glu Pro Glu Glu Arg His Thr Glu Leu
263 545      550      555

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266 <210> SEQ ID NO: 7
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268 <212> TYPE: PRT
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276           20           25           30
278 Ile Arg Thr Thr His Thr Gly Gln Val Leu Gly Ser Leu Val His Val
279           35           40           45
281 Lys Gly Ala Asn Ala Gly Val Gln Thr Phe Leu Gly Ile Pro Phe Ala
282           50           55           60
284 Lys Pro Pro Leu Gly Pro Leu Arg Phe Ala Pro Pro Glu Pro Pro Glu
285   65           70           75           80
287 Ser Trp Ser Gly Val Arg Asp Gly Thr Thr His Pro Ala Met Cys Leu
288           85           90           95
290 Gln Asp Leu Thr Ala Val Glu Ser Glu Phe Leu Ser Gln Phe Asn Met
291           100          105          110
293 Thr Phe Pro Ser Asp Ser Met Ser Glu Asp Cys Leu Tyr Leu Ser Ile
294           115          120          125
296 Tyr Thr Pro Ala His Ser His Glu Gly Ser Asn Leu Pro Val Met Val
297           130          135          140
299 Trp Ile His Gly Gly Ala Leu Val Phe Gly Met Ala Ser Leu Tyr Asp
300  145          150          155          160
302 Gly Ser Met Leu Ala Ala Leu Glu Asn Val Val Val Val Ile Ile Gln
303           165          170          175
305 Tyr Arg Leu Gly Val Leu Gly Phe Phe Ser Thr Gly Asp Lys His Ala
306           180          185          190
308 Thr Gly Asn Trp Gly Tyr Leu Asp Gln Val Ala Ala Leu Arg Trp Val
309           195          200          205
311 Gln Gln Asn Ile Ala His Phe Gly Gly Asn Pro Asp Arg Val Thr Ile
312           210          215          220
314 Phe Gly Glu Ser Ala Gly Gly Thr Ser Val Ser Ser Leu Val Val Ser
315  225          230          235          240
317 Pro Ile Ser Gln Gly Leu Phe His Gly Ala Ile Met Glu Ser Gly Val
318           245          250          255
320 Ala Leu Leu Pro Gly Leu Ile Ala Ser Ser Ala Asp Val Ile Ser Thr
321           260          265          270
323 Val Val Ala Asn Leu Ser Ala Cys Asp Gln Val Asp Ser Glu Ala Leu
324           275          280          285
326 Val Gly Cys Leu Arg Gly Lys Ser Lys Glu Glu Ile Leu Ala Ile Asn
327           290          295          300
329 Lys Pro Phe Lys Met Ile Pro Gly Val Val Asp Gly Val Phe Leu Pro
330  305          310          315          320
332 Arg His Pro Gln Glu Leu Leu Ala Ser Ala Asp Phe Gln Pro Val Pro
333           325          330          335
335 Ser Ile Val Gly Val Asn Asn Asn Glu Phe Gly Trp Leu Ile Pro Lys
336           340          345          350

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VERIFICATION SUMMARY

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